

## SEQUENCE LISTING

<110> Reinherz, Ellis L.  
 Freund, Christian  
 Li, Jing  
 Nishizawa, Kazuhisa  
 Wagner, Gerhard

<120> Cloning and Characterization of a CD2  
 Binding Protein (CD2BP2)

<130> 1062.1021-004

<150> US 60/111,007

<151> 1998-12-04

<150> US 60/115,647

<151> 1999-01-13

<150> PCT/US99/26993

<151> 1999-11-15

<160> 25

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1299

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (121)...(1143)

<400> 1

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atg cca aag agg aaa gtg acc ttc caa ggc gtg gga gat gag gag gat      168
Met Pro Lys Arg Lys Val Thr Phe Gln Gly Val Gly Asp Glu Glu Asp
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gag gat gaa atc att gtc ccc aag aag aag ctg gtg gac cct gtg gct      216
Glu Asp Glu Ile Ile Val Pro Lys Lys Lys Leu Val Asp Pro Val Ala
           20             25             30

ggg tca ggg ggt cct ggg agc cgc ttt aaa ggc aaa cac tct ttg gat      264
Gly Ser Gly Gly Pro Gly Ser Arg Phe Lys Gly Lys His Ser Leu Asp
           35             40             45

agc gat gag gag gag gat gat gat gat ggg ggg tcc agc aaa tat gac      312
Ser Asp Glu Glu Glu Asp Asp Asp Asp Gly Gly Ser Ser Lys Tyr Asp
           50             55             60

atc ttg gcc tca gag gat gta gaa ggt cag gag gca gcc aca ctc ccc      360
Ile Leu Ala Ser Glu Asp Val Glu Gly Gln Glu Ala Ala Thr Leu Pro
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gag Glu	gaa Glu	ggc Gly	cac His 100	ttt Phe	gat Asp	gcc Ala	gat Asp	ggc Gly 105	aac Asn	tac Tyr	ttc Phe	ctg Leu	aac Asn 110	cgg Arg	gat Asp	456
gct Ala	cag Gln	atc Ile 115	cga Arg	gac Asp	agc Ser	tgg Trp	ctg Leu 120	gac Asp	aac Asn	att Ile	gac Asp	tgg Trp 125	gtg Val	aag Lys	atc Ile	504
cgg Arg	gag Glu 130	cgg Arg	cca Pro	cct Pro	ggc Gly	cag Gln 135	cgc Arg	cag Gln	gcc Ala	tca Ser	gac Asp 140	tcg Ser	gag Glu	gag Glu	gag Glu	552
gac Asp 145	agc Ser	ttg Leu	ggc Gly	cag Gln	acc Thr 150	tca Ser	atg Met	agt Ser	gcc Ala	caa Gln 155	gcc Ala	ctc Leu	ttg Leu	gag Glu	gga Gly 160	600
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cgt Arg	ctg Leu	ggg Gly	gcc Ala 180	cga Arg	gga Gly	gga Gly	ggc Gly	aaa Lys 185	ggg Gly	aga Arg	aag Lys	ggg Gly 190	cct Pro	ggg Gly	caa Gln	696
ccc Pro	agt Ser	tcc Ser 195	cct Pro	cag Gln	cgc Arg	ctg Leu	gac Asp 200	cgg Arg	ctc Leu	tcc Ser	ggg Gly 205	ttg Leu	gcc Ala	gac Asp	cag Gln	744
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ttg Leu 225	gct Ala	atg Met	cgt Arg	ctg Leu	aag Lys 230	ggt Gly	ttg Leu	ggg Gly	tgt Cys	cag Gln 235	acc Thr	cta Leu	gga Gly	ccc Pro	cac His 240	840
aat Asn	ccc Pro	aca Thr	ccc Pro	cca Pro 245	ccc Pro	tcc Ser	ctg Leu	gac Asp	atg Met 250	ttc Phe	gct Ala	gag Glu	gag Glu	ttg Leu 255	gcg Ala	888
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aac Asn	acg Thr 290	ggg Gly	gat Asp	gcc Ala	gag Glu	ctg Leu 295	tat Tyr	ggg Gly	ccc Pro	ttc Phe	acc Thr 300	agc Ser	gcc Ala	cag Gln	atg Met	1032

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 305 310 315 320

aag ctg gac ccc cct ggt ggt cag ttc tac aac tcc aaa cgc att gac 1128  
 Lys Leu Asp Pro Pro Gly Gly Gln Phe Tyr Asn Ser Lys Arg Ile Asp  
 325 330 335

ttt gac ctc tac acc tgagcctgct gggggcccag tttggtgggc ctttctttcc 1183  
 Phe Asp Leu Tyr Thr  
 340

tggactttgt ggaggaggca ccaagtgtct caggcagcga ggaaattgga ggccattttt 1243  
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 <213> Homo sapiens

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 35 40 45  
 Ser Asp Glu Glu Glu Asp Asp Asp Gly Gly Ser Ser Lys Tyr Asp  
 50 55 60  
 Ile Leu Ala Ser Glu Asp Val Glu Gly Gln Glu Ala Ala Thr Leu Pro  
 65 70 75 80  
 Ser Glu Gly Gly Gly Arg Ile Thr Pro Phe Asn Leu Gln Glu Glu Met  
 85 90 95  
 Glu Glu Gly His Phe Asp Ala Asp Gly Asn Tyr Phe Leu Asn Arg Asp  
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 Ala Gln Ile Arg Asp Ser Trp Leu Asp Asn Ile Asp Trp Val Lys Ile  
 115 120 125  
 Arg Glu Arg Pro Pro Gly Gln Arg Gln Ala Ser Asp Ser Glu Glu Glu  
 130 135 140  
 Asp Ser Leu Gly Gln Thr Ser Met Ser Ala Gln Ala Leu Leu Glu Gly  
 145 150 155 160  
 Leu Leu Glu Leu Leu Leu Pro Arg Glu Thr Val Ala Gly Ala Leu Arg  
 165 170 175  
 Arg Leu Gly Ala Arg Gly Gly Gly Lys Gly Arg Lys Gly Pro Gly Gln  
 180 185 190  
 Pro Ser Ser Pro Gln Arg Leu Asp Arg Leu Ser Gly Leu Ala Asp Gln  
 195 200 205  
 Met Val Ala Arg Gly Asn Leu Gly Val Tyr Gln Glu Thr Arg Glu Arg  
 210 215 220  
 Leu Ala Met Arg Leu Lys Gly Leu Gly Cys Gln Thr Leu Gly Pro His  
 225 230 235 240  
 Asn Pro Thr Pro Pro Pro Ser Leu Asp Met Phe Ala Glu Glu Leu Ala  
 245 250 255  
 Glu Glu Glu Leu Glu Thr Pro Thr Pro Thr Gln Arg Gly Glu Ala Glu  
 260 265 270  
 Ser Arg Gly Asp Gly Leu Val Asp Val Met Trp Glu Tyr Lys Trp Glu  
 275 280 285  
 Asn Thr Gly Asp Ala Glu Leu Tyr Gly Pro Phe Thr Ser Ala Gln Met  
 290 295 300

Gln Thr Trp Val Ser Glu Gly Tyr Phe Pro Asp Gly Val Tyr Cys Arg  
 305 310 315 320  
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 325 330 335  
 Phe Asp Leu Tyr Thr  
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<210> 3  
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 <212> PRT  
 <213> Homo sapiens

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 Trp Val Ser Glu Gly Tyr Phe Pro Asp Gly  
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<210> 4  
 <211> 27  
 <212> PRT  
 <213> Caenorhabditis elegans

<400> 4  
 Gly Pro Asp Ser Glu Lys Tyr Gly Pro Tyr Met Ser Lys Asp Met Leu  
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 Phe Trp Leu Gln Ala Gly Tyr Phe Asn Asp Gly  
 20 25

<210> 5  
 <211> 27  
 <212> PRT  
 <213> Caenorhabditis elegans

<400> 5  
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 1 5 10 15  
 Val Trp Phe Lys Ala Gly Tyr Phe Thr Asp Glu  
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<210> 6  
 <211> 27  
 <212> PRT  
 <213> Caenorhabditis elegans

<400> 6  
 Asp Asp Arg Gly Thr Val Gln Gly Pro Tyr Gly Ala Ser Thr Val Leu  
 1 5 10 15  
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 20 25

<210> 7  
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 <212> PRT

<213> *Saccharomyces cerevisiae*

<400> 7

Asp	Thr	Gln	Gly	Gln	Ile	His	Gly	Pro	Phe	Thr	Thr	Gln	Met	Met	Ser
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Gln	Trp	Tyr	Ile	Gly	Gly	Leu	Glu	Tyr	Phe	Ala	Ser	Thr			
			20					25							

<210> 8

<211> 27

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 8

Asp	Ser	Asn	Gly	Asn	Ile	Gln	Gly	Pro	Phe	Gly	Thr	Asn	Asn	Met	Ser
1				5					10					15	
Gln	Trp	Tyr	Gln	Gly	Gly	Tyr	Phe	Thr	Pro	Thr					
			20					25							

<210> 9

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Motif in CD2 binding region of CD2BP2

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<222> (1)...(2)

<223> Xaa = Any Amino Acid

<221> VARIANT

<222> (3)...(3)

<223> Xaa can be Tyr or Phe

<221> VARIANT

<222> (4)...(7)

<223> Xaa = Any Amino Acid

<221> VARIANT

<222> (8)...(8)

<223> Xaa can be Met or Val

<221> VARIANT

<222> (9)...(15)

<223> Xaa = Any Amino Acid

<400> 9

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Phe															

<210> 10

<211> 6

<212> PRT  
 <213> Artificial Sequence  
 <220>  
 <223> CD2BP2 binding region

<400> 10  
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<210> 11  
 <211> 70  
 <212> PRT  
 <213> Homo sapiens

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 Pro Pro Pro Gly His Arg Val Gln His Gln Pro Gln Lys Arg Pro Pro  
 20 25 30  
 Ala Pro Ser Gly Thr Gln Val His Gln Gln Lys Gly Pro Pro Leu Pro  
 35 40 45  
 Arg Pro Arg Val Gln Pro Lys Pro Pro His Gly Ala Ala Glu Asn Ser  
 50 55 60  
 Leu Ser Pro Ser Ser Asn  
 65 70

<210> 12  
 <211> 8  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Kozak consensus sequence

<400> 12  
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8

<210> 13  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

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 <223> Flag Epitope

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24

<210> 14  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Flag Epitope

<400> 14  
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<210> 15  
 <211> 31  
 <212> PRT  
 <213> Gallus gallus

<220>  
 <223> Flag Epitope

<400> 15  
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 Gln Glu Met Ala Glu Trp Phe Gln Ala Gly Tyr Phe Thr Met Ser  
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<210> 16  
 <211> 38  
 <212> PRT  
 <213> Drosophila melanogaster

<220>  
 <223> Flag Epitope

<400> 16  
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 Gly Pro Phe Ser Thr Glu Lys Met Leu Lys Trp Ser Gln Glu Asn Thr  
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 Arg Tyr Phe Lys Asn Gly  
 35

<210> 17  
 <211> 34  
 <212> PRT  
 <213> Leishmania major

<220>  
 <223> Flag Epitope

<400> 17  
 Val Trp Met Met Arg Trp Lys Ala Lys Pro Thr Val Gln His Gly Pro  
 1 5 10 15  
 Phe Thr Asp Asp Ala Ile Gln Gln Trp Gly Arg Asp Gly Tyr Phe Gly  
 20 25 30  
 Lys Lys

<210> 18  
 <211> 36  
 <212> PRT  
 <213> Caenorhabditis elegans

&lt;220&gt;

&lt;223&gt; Flag Epitope

&lt;400&gt; 18

Val	Ile	Asp	Thr	Lys	Trp	His	Tyr	Leu	Gly	Pro	Asp	Ser	Glu	Lys	Tyr
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Gly	Pro	Tyr	Met	Ser	Lys	Asp	Met	Leu	Phe	Trp	Leu	Gln	Ala	Gly	Tyr
			20					25					30		
Phe	Asn	Asp	Gly												
			35												

&lt;210&gt; 19

&lt;211&gt; 35

&lt;212&gt; PRT

<213> *Caenorhabditis elegans*

&lt;220&gt;

&lt;223&gt; Flag Epitope

&lt;400&gt; 19

Val	Glu	Ser	Ser	Trp	Arg	Tyr	Ile	Asp	Thr	Gln	Gly	Gln	Ile	His	Gly
1				5					10					15	
Pro	Phe	Thr	Ile	Gln	Met	Met	Ser	Gln	Trp	Tyr	Ile	Gly	Gly	Tyr	Phe
			20					25					30		
Ala	Ser	Thr													
			35												

&lt;210&gt; 20

&lt;211&gt; 35

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;220&gt;

&lt;223&gt; Flag Epitope

&lt;400&gt; 20

Ile	Glu	Ser	Gln	Trp	Lys	Tyr	Ile	Asp	Ser	Asn	Gly	Asn	Ile	Gln	Gly
1				5					10					15	
Pro	Phe	Gly	Thr	Asn	Asn	Met	Ser	Gln	Trp	Tyr	Gln	Gly	Gly	Tyr	Phe
			20					25					30		
Thr	Pro	Thr													
			35												

&lt;210&gt; 21

&lt;211&gt; 31

&lt;212&gt; PRT

<213> *Saccharomces pombe*

&lt;220&gt;

&lt;223&gt; Flag Epitope

&lt;400&gt; 21

Trp	Leu	Tyr	Lys	Asp	Pro	Gln	Asn	Asn	Val	Gln	Gly	Pro	Phe	Thr	Gly
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Val	Asp	Met	His	Gln	Trp	Tyr	Arg	Ala	Gly	Tyr	Phe	Pro	Leu	Gly	
			20					25					30		



<210> 22  
 <211> 21  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Flag Epitope

<400> 22  
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 1 5 10 15  
 Pro Pro Gly His Arg  
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<210> 23  
 <211> 62  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Flag Epitope

<400> 23  
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 Tyr Gly Pro Phe Thr Ser Ala Gln Met Gln Thr Trp Val Ser Glu Gly  
 20 25 30  
 Tyr Phe Pro Asp Gly Val Tyr Cys Arg Lys Leu Asp Pro Pro Gly Gly  
 35 40 45  
 Gln Phe Tyr Asn Ser Lys Arg Ile Asp Phe Asp Leu Tyr Thr  
 50 55 60

<210> 24  
 <211> 31  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Flag Epitope

<400> 24  
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 1 5 10 15  
 Gln Glu Met Ala Glu Trp Phe Gln Ala Gly Tyr Phe Thr Met Ser  
 20 25 30

<210> 25  
 <211> 31  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Flag Epitope

<400> 25

10/10

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Gln	Glu	Met	Ala	Glu	Trp	Phe	Gln	Ala	Gly	Tyr	Phe	Ser	Met	Ser	
			20					25					30		